

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
MacBeth, Kyle J.
Williamson, Mark

<120> 22012, A Novel Human Carboxypeptidase

<130> 5800-38

<160> 4

<170> FastSEQ for Windows Version 3.0

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<211> 492

<212> PRT

<213> Homo sapiens

<400> 1

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Glu Arg Phe Phe Gln Gln Arg Leu Asp His Phe Asn Phe Glu Arg Phe
 35          40          45
Gly Asn Lys Thr Phe Pro Gln Arg Phe Leu Val Ser Asp Arg Phe Trp
 50          55          60
Val Arg Gly Glu Gly Pro Ile Phe Phe Tyr Thr Gly Asn Glu Gly Asp
 65          70          75          80
Val Trp Ala Phe Ala Asn Asn Ser Gly Phe Val Ala Glu Leu Ala Ala
 85          90          95
Glu Arg Gly Ala Leu Leu Val Phe Ala Glu His Arg Tyr Tyr Gly Lys
100          105          110
Ser Leu Pro Phe Gly Ala Gln Ser Thr Gln Arg Gly His Thr Glu Leu
115          120          125
Leu Thr Val Glu Gln Ala Leu Ala Asp Phe Ala Glu Leu Leu Arg Ala
130          135          140
Leu Arg Arg Asp Leu Gly Ala Gln Asp Ala Pro Ala Ile Ala Phe Gly
145          150          155          160
Gly Ser Tyr Gly Gly Met Leu Ser Ala Tyr Leu Arg Met Lys Tyr Pro
165          170          175
His Leu Val Ala Gly Ala Leu Ala Ala Ser Ala Pro Val Leu Ala Val
180          185          190
Ala Gly Leu Gly Asp Ser Asn Gln Phe Phe Arg Asp Val Thr Ala Asp
195          200          205
Phe Glu Gly Gln Ser Pro Lys Cys Thr Gln Gly Val Arg Glu Ala Phe
210          215          220
Arg Gln Ile Lys Asp Leu Phe Leu Gln Gly Ala Tyr Asp Thr Val Arg
225          230          235          240
Trp Glu Phe Gly Thr Cys Gln Pro Leu Ser Asp Glu Lys Asp Leu Thr
245          250          255
Gln Leu Phe Met Phe Ala Arg Asn Ala Phe Thr Val Leu Ala Met Met
260          265          270
Asp Tyr Pro Tyr Pro Thr Asp Phe Leu Gly Pro Leu Pro Ala Asn Pro

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cgc tac tac ggg aag tcg ctg ccg ttc ggt gcg cag tcc acg cag cgc Arg Tyr Tyr Gly Lys Ser Leu Pro Phe Gly Ala Gln Ser Thr Gln Arg 110 115 120	387
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gcc atc gcc ttc ggt gga agt tat ggg ggg atg ctc agt gcc tac ctg Ala Ile Ala Phe Gly Gly Ser Tyr Gly Gly Met Leu Ser Ala Tyr Leu 160 165 170	531
agg atg aag tat ccc cac ctg gtg gcg ggg gcg ctg gcg gcc agc gcg Arg Met Lys Tyr Pro His Leu Val Ala Gly Ala Leu Ala Ser Ala 175 180 185	579
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gcc cag agg atc acg ggg ctg cga gca ctg gca ggg ctg gtc tac aac	963
Ala Gln Arg Ile Thr Gly Leu Arg Ala Leu Ala Gly Leu Val Tyr Asn	
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gcc tcg ggc tcc gag cac tgc tac gac atc tac cgg ctc tac cac agc	1011
Ala Ser Gly Ser Glu His Cys Tyr Asp Ile Tyr Arg Leu Tyr His Ser	
320 325 330	
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Cys Ala Asp Pro Thr Gly Cys Gly Thr Gly Pro Asp Ala Arg Ala Trp	
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gac tac cag gcc tgc acc gag atc aac ctg acc ttc gcc agc aac aat	1107
Asp Tyr Gln Ala Cys Thr Glu Ile Asn Leu Thr Phe Ala Ser Asn Asn	
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gtg acc gat atg ttc ccc gag ctg ccc ttc act gac gag ctc cgc cag	1155
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Leu Thr Ser Phe Trp Gly Gly Asp Leu Arg Ala Ala Ser Asn Ile Ile	
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Phe Ser Asn Gly Asn Leu Asp Pro Trp Ala Gly Gly Gly Ile Arg Arg	
415 420 425	
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Asn Leu Ser Ala Ser Val Ile Ala Val Thr Ile Gln Gly Gly Ala His	
430 435 440	
cac ctc gac ctc aga gcc tcc cac cca gaa gat cct gct tcc gtg gtt	1395
His Leu Asp Leu Arg Ala Ser His Pro Glu Asp Pro Ala Ser Val Val	
445 450 455	
gag gcg cgg aag ctg gag gcc acc atc atc ggc gag tgg gta aag gca	1443
Glu Ala Arg Lys Leu Glu Ala Thr Ile Ile Gly Glu Trp Val Lys Ala	
460 465 470 475	
gcc agg cgt gag cag cag cca gct ctg cgt ggg ggg ccc aga ctc agc	1491
Ala Arg Arg Glu Gln Pro Ala Leu Arg Gly Gly Pro Arg Leu Ser	
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ctc tgagcacagg actggagggg tctcaaggct cctcatggag tgggggcttc	1544
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<220>
 <223> consensus sequence for the prolyloligopeptidase
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 35 40 45
 Gly His Ser Met Gly Gly Ala Leu Ala Ala Ala Tyr Ala Ala Lys Tyr
 50 55 60
 Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro
 65 70 75 80
 Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly
 85 90 95
 Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala
 100 105 110
 Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe
 115 120 125
 Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala
 130 135 140
 Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Leu Gly Tyr Ala Val
 145 150 155 160
 Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile
 165 170 175
 Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro
 180 185 190
 Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val
 195 200 205
 Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu
 210 215 220
 Glu Val Ala Glu Leu Ile Lys Phe Leu Ala Leu Ser Thr Asn Asx Ile
 225 230 235 240
 Arg Asp Ala Leu Ser Thr Asn Asx Ile Arg Asp
 245 250